



## SEQUENCE LISTING

<110> Kingsbury, G.  
Leiby, K.

<120> COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND  
TREATMENT OF IMMUNE DISORDERS

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<150> 60/155,862

<151> 1999-09-24

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Thr	Tyr	Pro	Val	Glu	Trp	Tyr	Ser	Asp	Thr	Asn	Glu	Ser	Ile	Pro	
	50					55				60					
Thr	Gln	Lys	Arg	Asn	Arg	Ile	Phe	Val	Ser	Arg	Asp	Arg	Leu	Lys	Phe
65					70					75					80
Leu	Pro	Ala	Arg	Val	Glu	Asp	Ser	Gly	Ile	Tyr	Ala	Cys	Val	Ile	Arg
				85					90					95	
Ser	Pro	Asn	Leu	Asn	Lys	Thr	Gly	Tyr	Leu	Asn	Val	Thr	Ile	His	Lys
		100						105					110		
Lys	Pro	Pro	Ser	Cys	Asn	Ile	Pro	Asp	Tyr	Leu	Met	Tyr	Ser	Thr	Val
		115					120					125			
Arg	Gly	Ser	Asp	Lys	Asn	Phe	Lys	Ile	Thr	Cys	Pro	Thr	Ile	Asp	Leu
	130					135					140				
Tyr	Asn	Trp	Thr	Ala	Pro	Val	Gln	Trp	Phe	Lys	Asn	Cys	Lys	Ala	Leu
145					150					155					160
Gln	Glu	Pro	Arg	Phe	Arg	Ala	His	Arg	Ser	Tyr	Leu	Phe	Ile	Asp	Asn
				165					170					175	
Val	Thr	His	Asp	Asp	Glu	Gly	Asp	Tyr	Thr	Cys	Gln	Phe	Thr	His	Ala
			180					185					190		
Glu	Asn	Gly	Thr	Asn	Tyr	Ile	Val	Thr	Ala	Thr	Arg	Ser	Phe	Thr	Val
		195					200					205			
Glu	Glu	Lys	Gly	Phe	Ser	Met	Phe	Pro	Val	Ile	Thr	Asn	Pro	Pro	Tyr
	210					215					220				

Asn	His	Thr	Met	Glu	Val	Glu	Ile	Gly	Lys	Pro	Ala	Ser	Ile	Ala	Cys
225					230					235					240
Ser	Ala	Cys	Phe	Gly	Lys	Gly	Ser	His	Phe	Leu	Ala	Asp	Val	Leu	Trp
				245					250						255
Gln	Ile	Asn	Lys	Thr	Val	Val	Gly	Asn	Phe	Gly	Glu	Ala	Arg	Ile	Gln
			260					265					270		
Glu	Glu	Glu	Gly	Arg	Asn	Glu	Ser	Ser	Ser	Asn	Asp	Met	Asp	Cys	Leu
		275					280					285			
Thr	Ser	Val	Leu	Arg	Ile	Thr	Gly	Val	Thr	Glu	Lys	Asp	Leu	Ser	Leu
	290					295					300				
Glu	Tyr	Asp	Cys	Leu	Ala	Leu	Asn	Leu	His	Gly	Met	Ile	Arg	His	Thr
305					310					315					320
Ile	Arg	Leu	Arg	Arg	Lys	Gln	Pro	Ile	Asp	His	Arg	Ser	Ile	Tyr	Tyr
				325					330					335	
Ile	Val	Ala	Gly	Cys	Ser	Leu	Leu	Leu	Met	Phe	Ile	Asn	Val	Leu	Val
			340					345					350		
Ile	Val	Leu	Lys	Val	Phe	Trp	Ile	Glu	Val	Ala	Leu	Phe	Trp	Arg	Asp
		355					360					365			
Ile	Val	Thr	Pro	Tyr	Lys	Thr	Arg	Asn	Asp	Gly	Lys	Leu	Tyr	Asp	Ala
	370					375					380				
Tyr	Ile	Ile	Tyr	Pro	Arg	Val	Phe	Arg	Gly	Ser	Ala	Ala	Gly	Thr	His
385					390					395					400
Ser	Val	Glu	Tyr	Phe	Val	His	His	Thr	Leu	Pro	Asp	Val	Leu	Glu	Asn
				405					410					415	
Lys	Cys	Gly	Tyr	Lys	Leu	Cys	Ile	Tyr	Gly	Arg	Asp	Leu	Leu	Pro	Gly
			420					425					430		
Gln	Asp	Ala	Ala	Thr	Val	Val	Glu	Ser	Ser	Ile	Gln	Asn	Ser	Arg	Arg
			435				440					445			
Gln	Val	Phe	Val	Leu	Ala	Pro	His	Met	Met	His	Ser	Lys	Glu	Phe	Ala
	450					455					460				
Tyr	Glu	Gln	Glu	Ile	Ala	Leu	His	Ser	Ala	Leu	Ile	Gln	Asn	Asn	Ser
465					470					475					480
Lys	Val	Ile	Leu	Ile	Glu	Met	Glu	Pro	Leu	Gly	Glu	Ala	Ser	Arg	Leu
			485						490					495	
Gln	Val	Gly	Asp	Leu	Gln	Asp	Ser	Leu	Gln	His	Leu	Val	Lys	Ile	Gln
			500					505					510		
Gly	Thr	Ile	Lys	Trp	Arg	Glu	Asp	His	Val	Ala	Asp	Lys	Gln	Ser	Leu
	515						520					525			
Ser	Ser	Lys	Phe	Trp	Lys	His	Val	Arg	Tyr	Gln	Met	Pro	Val	Pro	Glu
	530					535					540				
Arg	Ala	Ser	Lys	Thr	Ala	Ser	Val	Ala	Ala	Pro	Leu	Ser	Gly	Lys	Ala
545					550					555					560
Cys	Leu	Asp	Leu	Lys	His	Phe									
				565											

<210> 8  
 <211> 556  
 <212> PRT  
 <213> Homo sapiens

<400> 8															
Met	Gly	Phe	Trp	Ile	Leu	Ala	Ile	Leu	Thr	Ile	Leu	Met	Tyr	Ser	Thr
1				5					10				15		
Ala	Ala	Lys	Phe	Ser	Lys	Gln	Ser	Trp	Gly	Leu	Glu	Asn	Glu	Ala	Leu
			20					25					30		
Ile	Val	Arg	Cys	Pro	Arg	Gln	Gly	Lys	Pro	Ser	Tyr	Thr	Val	Asp	Trp
		35					40					45			
Tyr	Tyr	Ser	Gln	Thr	Asn	Lys	Ser	Ile	Pro	Thr	Gln	Glu	Arg	Asn	Arg
	50				55						60				
Val	Phe	Ala	Ser	Gly	Gln	Leu	Leu	Lys	Phe	Leu	Pro	Ala	Glu	Val	Ala
65					70					75					80

Asp	Ser	Gly	Ile	Tyr	Thr	Cys	Ile	Val	Arg	Ser	Pro	Thr	Phe	Asn	Arg		
			85						90					95			
Thr	Gly	Tyr	Ala	Asn	Val	Thr	Ile	Tyr	Lys	Lys	Gln	Ser	Asp	Cys	Asn		
			100					105					110				
Val	Pro	Asp	Tyr	Leu	Met	Tyr	Ser	Thr	Val	Ser	Gly	Ser	Glu	Lys	Asn		
		115					120					125					
Ser	Lys	Ile	Tyr	Cys	Pro	Thr	Ile	Asp	Leu	Tyr	Asn	Trp	Thr	Ala	Pro		
	130					135					140						
Leu	Glu	Trp	Phe	Lys	Asn	Cys	Gln	Ala	Leu	Gln	Gly	Ser	Arg	Tyr	Arg		
145					150					155					160		
Ala	His	Lys	Ser	Phe	Leu	Val	Ile	Asp	Asn	Val	Met	Thr	Glu	Asp	Ala		
			165						170					175			
Gly	Asp	Tyr	Thr	Cys	Lys	Phe	Ile	His	Asn	Glu	Asn	Gly	Ala	Asn	Tyr		
		180						185					190				
Ser	Val	Thr	Ala	Thr	Arg	Ser	Phe	Thr	Val	Lys	Asp	Glu	Gln	Gly	Phe		
	195						200					205					
Ser	Leu	Phe	Pro	Val	Ile	Gly	Ala	Pro	Ala	Gln	Asn	Glu	Ile	Lys	Glu		
	210					215					220						
Val	Glu	Ile	Gly	Lys	Asn	Ala	Asn	Leu	Thr	Cys	Ser	Ala	Cys	Phe	Gly		
225					230					235					240		
Lys	Gly	Thr	Gln	Phe	Leu	Ala	Ala	Val	Leu	Trp	Gln	Leu	Asn	Gly	Thr		
			245						250					255			
Lys	Ile	Thr	Asp	Phe	Gly	Glu	Pro	Arg	Ile	Gln	Gln	Glu	Glu	Gly	Gln		
		260						265					270				
Asn	Gln	Ser	Phe	Ser	Asn	Gly	Leu	Ala	Cys	Leu	Asp	Met	Val	Leu	Arg		
	275					280						285					
Ile	Ala	Asp	Val	Lys	Glu	Glu	Asp	Leu	Leu	Leu	Gln	Tyr	Asp	Cys	Leu		
	290					295					300						
Ala	Leu	Asn	Leu	His	Gly	Leu	Arg	Arg	His	Thr	Val	Arg	Leu	Ser	Arg		
305					310					315					320		
Lys	Asn	Pro	Ile	Asp	His	His	Ser	Ile	Tyr	Cys	Ile	Ile	Ala	Val	Cys		
			325						330					335			
Ser	Val	Phe	Leu	Met	Leu	Ile	Asn	Val	Leu	Val	Ile	Ile	Leu	Lys	Met		
		340						345					350				
Phe	Trp	Ile	Glu	Ala	Thr	Leu	Leu	Trp	Arg	Asp	Ile	Ala	Lys	Pro	Tyr		
	355					360					365						
Lys	Thr	Arg	Asn	Asp	Gly	Lys	Leu	Tyr	Asp	Ala	Tyr	Val	Val	Tyr	Pro		
	370				375					380							
Arg	Asn	Tyr	Lys	Ser	Ser	Thr	Asp	Gly	Ala	Ser	Arg	Val	Glu	His	Phe		
385					390					395					400		
Val	His	Gln	Ile	Leu	Pro	Asp	Val	Leu	Glu	Asn	Lys	Cys	Gly	Tyr	Thr		
			405						410					415			
Leu	Cys	Ile	Tyr	Gly	Arg	Asp	Met	Leu	Pro	Gly	Glu	Asp	Val	Val	Thr		
		420						425					430				
Ala	Val	Glu	Thr	Asn	Ile	Arg	Lys	Ser	Arg	Arg	His	Ile	Phe	Ile	Leu		
	435						440					445					
Thr	Pro	Gln	Ile	Thr	His	Asn	Lys	Glu	Phe	Ala	Tyr	Glu	Gln	Glu	Val		
	450					455					460						
Ala	Leu	His	Cys	Ala	Leu	Ile	Gln	Asn	Asp	Ala	Lys	Val	Ile	Leu	Ile		
465					470					475					480		
Glu	Met	Glu	Ala	Leu	Ser	Glu	Leu	Asp	Met	Leu	Gln	Ala	Glu	Ala	Leu		
			485					490					495				
Gln	Asp	Ser	Leu	Gln	His	Leu	Met	Lys	Val	Gln	Gly	Thr	Ile	Lys	Trp		
		500						505					510				
Arg	Glu	Asp	His	Ile	Ala	Asn	Lys	Arg	Ser	Leu	Asn	Ser	Lys	Phe	Trp		
	515						520					525					
Lys	His	Val	Arg	Tyr	Gln	Met	Pro	Val	Pro	Ser	Lys	Ile	Pro	Arg	Lys		
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Ala	Ser	Ser	Leu	Thr	Pro	Leu	Ala	Ala	Gln	Lys	Gln						
545					550					555							

<210> 9  
 <211> 328  
 <212> PRT  
 <213> Homo sapiens

<400> 9  
 Met Gly Phe Trp Ile Leu Ala Ile Leu Thr Ile Leu Met Tyr Ser Thr  
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 Ala Ala Lys Phe Ser Lys Gln Ser Trp Gly Leu Glu Asn Glu Ala Leu  
 20 25 30  
 Ile Val Arg Cys Pro Arg Gln Gly Lys Pro Ser Tyr Thr Val Asp Trp  
 35 40 45  
 Tyr Tyr Ser Gln Thr Asn Lys Ser Ile Pro Thr Gln Glu Arg Asn Arg  
 50 55 60  
 Val Phe Ala Ser Gly Gln Leu Leu Lys Phe Leu Pro Ala Glu Val Ala  
 65 70 75 80  
 Asp Ser Gly Ile Tyr Thr Cys Ile Val Arg Ser Pro Thr Phe Asn Arg  
 85 90 95  
 Thr Gly Tyr Ala Asn Val Thr Ile Tyr Lys Lys Gln Ser Asp Cys Asn  
 100 105 110  
 Val Pro Asp Tyr Leu Met Tyr Ser Thr Val Ser Gly Ser Glu Lys Asn  
 115 120 125  
 Ser Lys Ile Tyr Cys Pro Thr Ile Asp Leu Tyr Asn Trp Thr Ala Pro  
 130 135 140  
 Leu Glu Trp Phe Lys Asn Cys Gln Ala Leu Gln Gly Ser Arg Tyr Arg  
 145 150 155 160  
 Ala His Lys Ser Phe Leu Val Ile Asp Asn Val Met Thr Glu Asp Ala  
 165 170 175  
 Gly Asp Tyr Thr Cys Lys Phe Ile His Asn Glu Asn Gly Ala Asn Tyr  
 180 185 190  
 Ser Val Thr Ala Thr Arg Ser Phe Thr Val Lys Asp Glu Gln Gly Phe  
 195 200 205  
 Ser Leu Phe Pro Val Ile Gly Ala Pro Ala Gln Asn Glu Ile Lys Glu  
 210 215 220  
 Val Glu Ile Gly Lys Asn Ala Asn Leu Thr Cys Ser Ala Cys Phe Gly  
 225 230 235 240  
 Lys Gly Thr Gln Phe Leu Ala Ala Val Leu Trp Gln Leu Asn Gly Thr  
 245 250 255  
 Lys Ile Thr Asp Phe Gly Glu Pro Arg Ile Gln Gln Glu Glu Gly Gln  
 260 265 270  
 Asn Gln Ser Phe Ser Asn Gly Leu Ala Cys Leu Asp Met Val Leu Arg  
 275 280 285  
 Ile Ala Asp Val Lys Glu Glu Asp Leu Leu Leu Gln Tyr Asp Cys Leu  
 290 295 300  
 Ala Leu Asn Leu His Gly Leu Arg Arg His Thr Val Arg Leu Ser Arg  
 305 310 315 320  
 Lys Asn Pro Ser Lys Glu Cys Phe  
 325

<210> 10  
 <211> 1680  
 <212> DNA  
 <213> Homo sapiens

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 ggctactctt cccaactcag tcttgaagag tatcaccaac tgcctcatgt gtggtgacct 120  
 tcaactgttg atgccagtga ctcatctgga gtaatctcaa caacgagtta ccaatacttg 180  
 ctcttgattg ataaacagaa tgggggtttg gatccttagca attctcacia ttctcatgta 240  
 ttccacagca gcaaagttaa gtaaacaatc atggggcctg gaaaatgagg ctttaattgt 300  
 aagatgtcct agacaaggaa aacctagtta caccgtggat tgggtattact cacaacaaaa 360



caaaagtatt	cccactcagg	aaagaaatcg	tgtgtttgcc	tcaggccgac	ttctgaagtt	420
tctaccagct	gaagttgctg	attctgggtat	ttatacctgt	attgtcagaa	gtccacatt	480
caataggact	ggatatgcga	atgtcaccat	atataaaaaa	caatcagatt	gcaatgttcc	540
agattatttg	atgtattcaa	cagtatctgg	atcagaaaaa	aattccaaaa	tttattgtcc	600
taccattgac	ctctacaact	ggacagcacc	tcttgagtgg	tttaagaatt	gtcaggctct	660
tcaaggatca	aggtacaggg	cgcacaagtc	atttttggtc	attgataatg	tgatgactga	720
ggacgcaggt	gattacacct	gtaaatttat	acacaatgaa	aatggagcca	attatagtgt	780
gacggcgacc	aggtccttca	cgggtcaaggt	ttggtgtcag	agtttctgca	aattaaaaaa	840
gagcttaatc	tttagtaata	ctcattggat	tcaaagtcta	atgagaggct	ttgtgatggg	900
atactatggg	gtacataaat	gttgtcgagt	ggtttttaat	ctttgtttgc	aatactttca	960
acatcatcaa	tggccttgaa	tgagcaaggc	ttttctctgt	ttccagtaat	cggagcccct	1020
gcacaaaatg	aaataaagga	agtggaaatt	ggaaaaaacg	caaacctaac	ttgctctgct	1080
tgttttggaa	aaggcactca	gttcttggct	gccgtcctgt	ggcagcttaa	tggaaacaaa	1140
attacagact	ttggtgaacc	aagaattcaa	caagaggaag	ggcaaaatca	aagtttcagc	1200
aatgggctgg	cttgtctaga	catggtttta	agaatagctg	acgtgaagga	agaggattta	1260
ttgctgcagt	acgactgtct	ggccctgaat	ttgcatggct	tgagaaggca	caccgtaaga	1320
ctaagtagga	aaaatccaag	taaggagtgt	ttctgagact	ttgatcacct	gaactttctc	1380
tagcaagtgt	aagcagaatg	gagtgtgggt	ccaagagatc	catcaagaca	atgggaatgg	1440
cctgtgccat	aaaatgtgct	tctcttcttc	gggatgttgt	ttgctgtctg	atctttgtag	1500
actgttcctg	tttgcctggga	gcttctctgc	tgcttaaatt	gttcgtcctc	ccccactccc	1560
tcctatcggt	ggtttgtcta	gaacactcag	ctgcttcttt	ggtcacccct	gttttctaac	1620
tttatgaact	ccctctgtgt	cactgtatgt	gaaaggaaat	gcaccaacaa	ccgaaaactg	1680

<210> 11  
 <211> 259  
 <212> PRT  
 <213> Homo sapiens

<400> 11

Met	Gly	Phe	Trp	Ile	Leu	Ala	Ile	Leu	Thr	Ile	Leu	Met	Tyr	Ser	Thr
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Ala	Ala	Lys	Phe	Ser	Lys	Gln	Ser	Trp	Gly	Leu	Glu	Asn	Glu	Ala	Leu
			20					25					30		
Ile	Val	Arg	Cys	Pro	Arg	Gln	Gly	Lys	Pro	Ser	Tyr	Thr	Val	Asp	Trp
		35					40					45			
Tyr	Tyr	Ser	Gln	Thr	Asn	Lys	Ser	Ile	Pro	Thr	Gln	Glu	Arg	Asn	Arg
	50				55						60				
Val	Phe	Ala	Ser	Gly	Arg	Leu	Leu	Lys	Phe	Leu	Pro	Ala	Glu	Val	Ala
65				70					75					80	
Asp	Ser	Gly	Ile	Tyr	Thr	Cys	Ile	Val	Arg	Ser	Pro	Thr	Phe	Asn	Arg
			85					90					95		
Thr	Gly	Tyr	Ala	Asn	Val	Thr	Ile	Tyr	Lys	Lys	Gln	Ser	Asp	Cys	Asn
			100					105					110		
Val	Pro	Asp	Tyr	Leu	Met	Tyr	Ser	Thr	Val	Ser	Gly	Ser	Glu	Lys	Asn
		115					120					125			
Ser	Lys	Ile	Tyr	Cys	Pro	Thr	Ile	Asp	Leu	Tyr	Asn	Trp	Thr	Ala	Pro
	130					135					140				
Leu	Glu	Trp	Phe	Lys	Asn	Cys	Gln	Ala	Leu	Gln	Gly	Ser	Arg	Tyr	Arg
145				150						155				160	
Ala	His	Lys	Ser	Phe	Leu	Val	Ile	Asp	Asn	Val	Met	Thr	Glu	Asp	Ala
			165					170						175	
Gly	Asp	Tyr	Thr	Cys	Lys	Phe	Ile	His	Asn	Glu	Asn	Gly	Ala	Asn	Tyr
		180					185					190			
Ser	Val	Thr	Ala	Thr	Arg	Ser	Phe	Thr	Val	Lys	Val	Trp	Cys	Gln	Ser
		195				200						205			
Phe	Cys	Lys	Leu	Lys	Lys	Ser	Leu	Ile	Phe	Ser	Asn	Thr	His	Trp	Ile
	210					215					220				
Gln	Ser	Leu	Met	Arg	Gly	Phe	Val	Met	Val	Tyr	Tyr	Gly	Val	His	Lys
225				230						235				240	
Cys	Cys	Arg	Val	Val	Phe	Asn	Leu	Cys	Leu	Gln	Tyr	Phe	Gln	His	His
			245					250						255	

Gln Trp Pro

<210> 12  
 <211> 1210  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (84)...(557)

<400> 12  
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 cttgctcttg attgataaac aga atg ggg ttt tgg atc tta gca att ctc aca 113  
 Met Gly Phe Trp Ile Leu Ala Ile Leu Thr  
 1 5 10

att ctc atg tat tcc aca gca gca aag ttt agt aaa caa tca tgg ggc 161  
 Ile Leu Met Tyr Ser Thr Ala Ala Lys Phe Ser Lys Gln Ser Trp Gly  
 15 20 25

ctg gaa aat gag gct tta att gta aga tgt cct aga caa gga aaa cct 209  
 Leu Glu Asn Glu Ala Leu Ile Val Arg Cys Pro Arg Gln Gly Lys Pro  
 30 35 40

agt tac acc gtg gat tgg tat tac tca caa aca aac aaa agt att ccc 257  
 Ser Tyr Thr Val Asp Trp Tyr Tyr Ser Gln Thr Asn Lys Ser Ile Pro  
 45 50 55

act cag gaa aga aat cgt gtg ttt gcc tca ggc caa ctt ctg aag ttt 305  
 Thr Gln Glu Arg Asn Arg Val Phe Ala Ser Gly Gln Leu Leu Lys Phe  
 60 65 70

cta cca gct gca gtt gct gat tct ggt att tat acc tgt att gtc aga 353  
 Leu Pro Ala Ala Val Ala Asp Ser Gly Ile Tyr Thr Cys Ile Val Arg  
 75 80 85 90

agt ccc aca ttc aat agg act gga tat gcg aat gtc acc ata tat aaa 401  
 Ser Pro Thr Phe Asn Arg Thr Gly Tyr Ala Asn Val Thr Ile Tyr Lys  
 95 100 105

aaa caa tca gat tgc aat gtt cca gat tat ttg atg tat tca aca gta 449  
 Lys Gln Ser Asp Cys Asn Val Pro Asp Tyr Leu Met Tyr Ser Thr Val  
 110 115 120

tct gga tca gaa aaa aat tcc aaa att tat tgt cct acc att gac ctc 497  
 Ser Gly Ser Glu Lys Asn Ser Lys Ile Tyr Cys Pro Thr Ile Asp Leu  
 125 130 135

tac aac tgg aca gca cct ctt gag tgg ttt aag atg agc aag gct ttt 545  
 Tyr Asn Trp Thr Ala Pro Leu Glu Trp Phe Lys Met Ser Lys Ala Phe  
 140 145 150

ctc tgt ttc cag taatcggagc ccctgcacaa aatgaaataa aggaagtgga 597  
 Leu Cys Phe Gln  
 155

aattggcact cagttcttgg ctgccgtcct gtggcagctt aatggaacaa aaattacaga 657  
 ctttggtgaa ccaagaattc aacaagagga agggcaaaat caaagtttca gcaatgggct 717  
 ggcttgtcta gacatggttt taagaatagc tgacgtgaag gaagaggatt tattgctgca 777

gtacgactgt ctggccctga atttgcatgg cttgagaagg cacaccgtaa gactaagtag 837  
gaaaaatcca agtaaggagt gtttctgaga ctttgatcac ctgaactttc tctagcaagt 897  
gtaagcagaa tggagtgtgg ttccaagaga tccatcaaga caatgggaat ggccctgtgcc 957  
ataaaatgtg cttctcttct tcgggatgtt gtttgctgtc tgatctttgt agactgttcc 1017  
tgtttgctgg gagcttctct gctgcttaaa ttgttcgtcc tccccactc cctcctatcg 1077  
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aagggcggcc gct 1210

<210> 13  
<211> 158  
<212> PRT  
<213> Homo sapiens

<400> 13  
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20 25 30  
Ile Val Arg Cys Pro Arg Gln Gly Lys Pro Ser Tyr Thr Val Asp Trp  
35 40 45  
Tyr Tyr Ser Gln Thr Asn Lys Ser Ile Pro Thr Gln Glu Arg Asn Arg  
50 55 60  
Val Phe Ala Ser Gly Gln Leu Leu Lys Phe Leu Pro Ala Ala Val Ala  
65 70 75 80  
Asp Ser Gly Ile Tyr Thr Cys Ile Val Arg Ser Pro Thr Phe Asn Arg  
85 90 95  
Thr Gly Tyr Ala Asn Val Thr Ile Tyr Lys Lys Gln Ser Asp Cys Asn  
100 105 110  
Val Pro Asp Tyr Leu Met Tyr Ser Thr Val Ser Gly Ser Glu Lys Asn  
115 120 125  
Ser Lys Ile Tyr Cys Pro Thr Ile Asp Leu Tyr Asn Trp Thr Ala Pro  
130 135 140  
Leu Glu Trp Phe Lys Met Ser Lys Ala Phe Leu Cys Phe Gln  
145 150 155

<210> 14  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> sense primer

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ttgccataga gagacctc 18

<210> 15  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense primer

<400> 15  
tgctgtccaa ttatacagg 19

<210> 16  
<211> 22  
<212> DNA

<213> Artificial Sequence  
 <220>  
 <223> sense primer  
 <400> 16  
 gaacacggca ttgtcactaa ct 22  
 <210> 17  
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 <223> antisense primer  
 <400> 17  
 cctcatagat gggcactgtg t 21  
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 <213> Artificial Sequence  
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 <400> 18  
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